

SEQUENCE LISTING

<110> Hevezi, Peter Mack, David Gish, Kurt C. Wilson, Keith E.

<120> NOVEL METHODS OF DIAGNOSIS OF PROSTATE AND/OR BREAST CANCER, COMPOSITIONS, AND METHODS OF SCREENING FOR PROSTATE CANCER AND/OR BREAST CANCER MODULATORS

<130> A-69199-1/DJB/JJD/AMS

<140> US 09/847,046

<141> 2001-04-30

<150> US 09/733,288

<151> 2000-12-08

<150> US 09/687,576

<151> 2000-10-13

<160> 3

<170> PatentIn version 3.1

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 $\mathcal{Q}^{\mathcal{V}}$

2640 ccgcaacatc tcaacgtggc actaggaaag ttcccaagtg tatgaaagaa acagatgtgc aggagaatga taaggaacaa catgaagata aatcggcagt cagaaaagaa ccgattgaaa 2700 ctctgagaat aaagcattgg aatagaagta attggtttaa agaagcagaa aaatcattta 2760 2820 gacgtgataa agagttagga tgctcaaaag tgaactaatt ttatagggct gtggtttcca 2880 aaattttttt ggcatgatag acttaattta tttccttaaa gaataatatt aaatcatttc 2940 aagtttgcag actagtgcca tccaatagaa ttataatata agtcacatat tttatttaaa attttctagt aactacatta aacaaagtaa aagtgagcag ggcaaaataa ttttgatatt 3000 acttttcacc cagtagtata cccaaaatag cgaaatatag aaattattaa tgagatattt 3060 tacatccttt tttgtaccaa gtcttctaaa tgcagtacat attttatact tactgcattt 3120 3180 cttacttccg agtagccata tttcaagtgt tcattgccac atgtggcctg tgactactgt 3240 attggacagt tcagtactag acaaaaacta gcataattaa cttagttcta gccatgattt ctatttggat taaaattaaa ctctaatcac agttaactcc acagtgcatt catgcagctg 3300 acagttatat ttgttttatt ggagtcatga tattaaaatc agcgtttgtc aacctcaggg 3360 3420 gatatttagc aattgtcggg agacattttt gatgtcatga ctagggcagt tattgacatt 3480 tagtgagtag aggccatgga tectgetaaa taacetgeat tggacagege eecacaacaa 3540 agaattatcc tgcccgaaat ggtagtcgtg ccaaggctga gtaaccttgt gttaaaagta 3600 acctgtggca gactaggttt ccagaatttc ctggttctgc tcacgtatca tgtttgaaaa aattttggct attaaagata tgtattagat ggtcttatcc tgattattac ctggatacaa 3660 3720 cttgatcttt tctaatattt tcagaaagtg atgggataac cctagaagag gactcagaat 3780 gatatttata ttttaagtga gtcttaaaac ctcctcttat ttctacaagt tatatggcta 3840 aatttcagat tgaacaggga ttcagcattc tgccatctcc tcatggaaag agaggctccc tcatctgaag cgtctctgaa atctaccctt gcaagcttca gacaaatcag ttgatctccc 3900 tgagccacac ggcctcattc tgtgagggag ggaaagatta gccaaagagt taattttcat 3960 4020 tccaaatcac ttagctgtta gactgatctg tttgtagcag ttgtttgtct catttttgct 4080 ctgtgcattt tttgagacat ttgttgagaa tattctattt ggtgctctac tgtatttttc tttttaatat ctacttgata tcttgttctt taaattttct tcacatatgg tttgcctgat 4140 acaactgatt tttataactg aaatttaagg aatctaacag ctaaaactca gtaagtgcat 4200 mtatttcctt ataacataga cccgttgcta ctctcagcac cctctcctca attttttttc 4260 ctgtagcatg tgatgcctga ttaaactcat tttcatttgc ttttatttct aatatgggaa 4320

 Q^{2}

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Pro Gln Lys Tyr Phe Ser Thr Leu Gln Pro Gly Leu Glu Glu Leu Asn 35 40 45

Glu Ala Val Arg Pro Leu Gln Asp Tyr Gly Ile Ser Val Ala Lys Val 50 55 60

Asn Cys Val Lys Glu Glu Ile Ser Arg Tyr Cys Gly Lys Glu Lys Asp 65 70 75 80

Leu Met Lys Ala Tyr Leu Phe Lys Gly Asn Ile Leu Leu Arg Glu Phe 85 90 95

Pro Thr Asp Thr Leu Phe Asp Val Asn Ala Ile Val Ala His Val Leu 100 105 110

Phe Ala Leu Leu Phe Ser Glu Val Lys Tyr Ile Thr Asn Leu Glu Asp 115 120 125

Leu Gln Asn Ile Glu Asn Ala Leu Lys Gly Lys Ala Asn Ile Ile Phe 130 135 140

Ser Tyr Val Arg Ala Ile Gly Ile Pro Glu His Arg Ala Val Met Glu 145 150 155 160

Ala Gly Phe Val Tyr Gly Thr Thr Tyr Gln Phe Val Leu Thr Thr Glu

165 170 175

Ile Ala Leu Leu Glu Ser Ile Gly Ser Glu Asp Val Glu Tyr Ala His 180 185 190

Leu Tyr Phe Phe His Cys Lys Leu Val Leu Asp Leu Thr Gln Gln Cys
195 200 205

Arg Arg Thr Leu Met Glu Gln Pro Leu Thr Thr Leu Asn Ile His Leu 210 215 220

Phe Ile Lys Thr Met Lys Ala Pro Leu Leu Thr Glu Val Ala Glu Asp 225 230 235 240

Pro Gln Gln Val Ser Thr Val His Leu Gln Leu Gly Leu Pro Leu Val 245 250 255

Phe Ile Val Ser Gln Gln Ala Thr Tyr Glu Ala Asp Arg Arg Thr Ala 260 265 270

Glu Trp Val Ala Trp Arg Leu Leu Gly Lys Ala Gly Val Leu Leu Leu 275 280 285

Leu Arg Asp Ser Leu Glu Val Asn Ile Pro Gln Asp Ala Asn Val Val 290 295 300

Phe Lys Arg Ala Glu Glu Gly Val Pro Val Glu Phe Leu Val Leu His 305 310 315 320

Asp Val Asp Leu Ile Ile Ser His Val Glu Asn Asn Met His Ile Glu 325 330 335

Glu Ile Gln Glu Asp Glu Asp Asn Asp Met Glu Gly Pro Asp Ile Asp 340 345 350

Val Gln Asp Asp Glu Val Ala Glu Thr Val Phe Arg Asp Arg Lys Arg 355 360 365

Lys Leu Pro Leu Glu Leu Thr Val Glu Leu Thr Glu Glu Thr Phe Asn 370 375 380

Ala Thr Val Met Ala Ser Asp Ser Ile Val Leu Phe Tyr Ala Gly Trp 385 390 395 400



Gln Ala Val Ser Met Ala Phe Leu Gln Ser Tyr Ile Asp Val Ala Val

Lys Leu Lys Gly Thr Ser Thr Met Leu Leu Thr Arg Ile Asn Cys Ala

Asp Trp Ser Asp Val Cys Thr Lys Gln Asn Val Thr Glu Phe Pro Ile

Ile Lys Met Tyr Lys Lys Gly Glu Asn Pro Val Ser Tyr Ala Gly Met 450 455

Leu Gly Thr Lys Asp Leu Leu Lys Phe Ile Gln Leu Asn Arg Ile Ser 470

Tyr Pro Val Asn Ile Thr Ser Ile Gln Glu Ala Glu Glu Tyr Leu Ser 490

Gly Glu Leu Tyr Lys Asp Leu Ile Leu Tyr Ser Ser Val Ser Val Leu 505

Gly Leu Phe Ser Pro Thr Met Lys Thr Ala Lys Glu Asp Phe Ser Glu 515 520

Ala Gly Asn Tyr Leu Lys Gly Tyr Val Ile Thr Gly Ile Tyr Ser Glu 530 535

Glu Asp Val Leu Leu Ser Thr Lys Tyr Ala Ala Ser Leu Pro Ala 545 550

Leu Leu Leu Ala Arg His Thr Glu Gly Lys Ile Glu Ser Ile Pro Leu 565 570

Ala Ser Thr His Ala Gln Asp Ile Val Gln Ile Ile Thr Asp Ala Leu 580

Leu Glu Met Phe Pro Glu Ile Thr Val Glu Asn Leu Pro Ser Tyr Phe 595 600

Arg Leu Gln Lys Pro Leu Leu Ile Leu Phe Ser Asp Gly Thr Val Asn 610 615 620

Pro Gln Tyr Lys Lys Ala Ile Leu Thr Leu Val Lys Gln Lys Tyr Leu









































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625 630 635 640

Asp Ser Phe Thr Pro Cys Trp Leu Asn Leu Lys Asn Thr Pro Val Gly 645 650 655

Arg Gly Ile Leu Arg Ala Tyr Phe Asp Pro Leu Pro Pro Leu Pro Leu 660 665 670

Leu Val Leu Val Asn Leu His Ser Gly Gly Gln Val Phe Ala Phe Pro 675 680 685

Ser Asp Gln Ala Ile Ile Glu Glu Asn Leu Val Leu Trp Leu Lys Lys 690 695 700

Leu Glu Ala Gly Leu Glu Asn His Ile Thr Ile Leu Pro Ala Gln Glu 705 710 715 720

Trp Lys Pro Pro Leu Pro Ala Tyr Asp Phe Leu Ser Met Ile Asp Ala 725 730 735

Ala Thr Ser Gln Arg Gly Thr Arg Lys Val Pro Lys Cys Met Lys Glu 740 745 750

Thr Asp Val Gln Glu Asn Asp Lys Glu Gln His Glu Asp Lys Ser Ala 755 760 765

Val Arg Lys Glu Pro Ile Glu Thr Leu Arg Ile Lys His Trp Asn Arg 770 775 780

Ser Asn Trp Phe Lys Glu Ala Glu Lys Ser Phe Arg Arg Asp Lys Glu 785 790 795 800

Leu Gly Cys Ser Lys Val Asn 805

<210> 3

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<212> PRT

<213> Unknown

<220>

<223> cytokine receptor extracellular motif found in many species

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<222> (3)..(3)

<223> "Xaa" at position 3 can be any amino acid.

<400> 3

Trp Ser Xaa Trp Ser 1 5

0